

Appl. No. : 09/816,763  
Filed : March 23, 2001

to the surface of the solid support by a spacer corresponding to or comprising at least a double-stranded DNA nucleotide sequence of at least 20 base pairs;

b. putting into contact said one or more transcriptional factor(s) with said bound double-stranded DNA sequence(s); and

c. identifying and/or quantifying a signal resulting from the binding of said transcriptional factor(s) upon said double-stranded DNA sequence(s).

#### REMARKS

Claim 9 has been canceled without prejudice and claim 1 has been amended. Support for the amendment can be found in prior claim 9 and the specification as filed, for example, on page 11, lines 8-12, the paragraph bridging pages 12 and 13, and page 13, lines 4-6.

As a result of this amendment, claims 1-8, 10, 12-22, 34 and 36-38 are pending for examination. The following addresses the substance of the Office Action:

#### Matters of obviousness

##### Peterson et al.

The Examiner has rejected Claims 1-10, 12-15, 17-22, 34 and 36-38 under 35 U.S.C. § 103(a) on the assertion that Peterson et al. make *prima facie* obvious the method embraced by the instant claims.

The present invention, as stated in claim 1 is directed to a screening and/or quantification method of one or more transcriptional factors(s) present in a cell or cell lysate, said method comprising the steps of:

a. binding to an insoluble solid support double-stranded DNA sequence(s) at the concentration of at least 0.01 pmole/cm<sup>2</sup> of said solid support surface, wherein the solid support is an array bearing at least 4 spots/cm<sup>2</sup> of solid support surface, each spot containing double-stranded DNA sequence(s) for the binding of transcriptional factor(s), said double-stranded DNA sequence comprising a specific sequence, said specific sequence being able to bind said one or more transcriptional factor(s) and said double-stranded DNA sequence being connected to the surface of the solid support by a spacer corresponding to or comprising at least a double-stranded DNA nucleotide sequence of at least 20 base pairs;

b. putting into contact said one or more transcriptional factor(s) with said bound double-stranded DNA sequence(s); and